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	-		1 MLQSLA(1 MLQSLA(/ Match Local Similarity nes 336; Conser	RESULT 1 S65566 inward rectifier potassium chanr C;Species: Homo sapiens (man) C;Date: 28-Oct-1996 #sequence_re C;Accession: S65566 R;Lesage, F:; Guillemare, E:; Fi EMBO J. 15, 1004-1011, 1996 A;Title: TWIK-1, a ubiquitous hu A;Reference number: S6556; MUJII A;Accession: S6556 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-336 CLES> A;Cross-references: EMBL:U33632;	204 199.5 199.5 199.5 190.5 190.5 190.5 190.5 190.5 190.5 188.5 188.5 188.5
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FRELYKIGITCYLLIGLIAMLVVLETFCELHELKKFRKMFYVKKI FSSITDQAAGMKEDQKQNEPFVATQSSACVDGPANH 336 	IVHAVLLGEVTVSCEFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQK	RRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGY	MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLK 	Score 1753; DB 2; Pred. No. 1.5e-146; 0; Mismatches 0;	TWIK-1 - human ion 13-Mar-1997 # M.; Duprat, F.; weakly inward re 183184 D:g1086490; PIDN:	126616 126953 126953 1721188 17214821 171584 1716629 1716629 1716629 1716426 1716426 1716426 1716426 1716426 1716426 1716426
DKDEDQVHIIEHDQLS 300		TSALFFASTVLSTTGY 120 TSALFFASTVLSTTGY 120 TSALFFASTVLSTTGY 120	ELPYEDLLRQELRKIK 60 	Length 336; Indels 0; Gaps .0;	7 #text_change 05-Nov-1999 .; Lazdunski, M.; Romey, G.; Barhani rectifying K(+) channel with a nove	hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable potassium hypothetical prote hypothetical prote hypothetical prote probable potassium hypothetical prote potassium channel potassium channel potassium channel potassium channel hypothetical prote potassium channel

RESULT 2
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hypothetical protein Y39B6B.f [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45032

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A;Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2
                                                                                                                                                                                  C; Genetics:
A; Gene: CESP: T28A8.1
                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, March 1997
A;Reference number: Z20027
A;Accession: T25392
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                                                                                                                                                                                                                 A;Cross-references: EMBL: 292813; PIDN: CAB07286.1; A; Experimental source: clone T28A8
                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-393 <WIL>
                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T28A8.1 - caenorhabditis elegans
C;Species: Caenorhabditis elegans
Tate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. Nature 368, 32-38, 1994

A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; £ A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. A;Recession: T45032

A;Accession: T45032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 3
A;Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3
A;Note: Y39B6B.f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AL132896; NID:g6434440; PIDN:CAB60911.1; PID:g6434446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-392 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: clone Y39B6B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
                                                                          Matches
                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atches 101;
                              12 RLVERHRSAWCFGFLVLGYLLYLVFGAVVFSSVELPYEDLLRQ---ELRKLKRRFLEEH- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 ETFCELHELKKFR-KMFYVKKDKD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 SIETDWSYLDAFYYCFVSLTTIGLGDFEPGDDPNQSFRGLYKIGATVYLMGGLCCMMLFL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 VLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLIGLIAMLVVL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 NWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 FSSVELPYEDLLRQELRKLKRRFLEE--HECLSEQQLEQFLGRVLEASNYGVSVLSNASG 98
           RIILAHVS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AT----LYDIPQFNLTSFFVKSDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---REP---SHKLRGLLNQRLGHLFTVNHIQLIHVGVVFASLLLFV----FAIPAWVFS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVTRRPVLYFHIRWGFSKQ-------VVAIVHAVLLGFVTVSCFFFIPAAVFS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPNWTFGQAFFFAGTLISTYGYGRYSPRTEYGKLFTILYCYIGIPLTLALLSAIVARM-- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSRIEYPLEKIEREAYLDYQNQWRDRLIQLDIDESEIDKLFLNIREAALNGIWMDRNLTS 177
                                                                         93;
                                                                                        Similarity
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                                                                       Conservative
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-LIVLSVVYVGFGAFLFYQLEQPNEVEVRARNIERFNIHKRQMIEHL
                                                                                   17.1%;
25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.6%; Score 430.5; DB 2; 38.3%; Pred. No. 3.2e-30;
                                                                    72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
                                                                Score 300; DB 2;
Pred. No. 9.4e-19;
'2; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365
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                                                                                                                                                                                                                           GSPDB:GN00021; CESP:T28A8.1
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                                                                                               Length 393;
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   62
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T27681
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A;Map position: 2
A;Introns: 51/3; 123/1; 212/1; 261/2; 331/3; 365/1; 394/2; 414/3
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z70038; PIDN:CAA93881.1; GSPDB:GN00020; CESP:ZK1067.5
A;Experimental source: clone ZK1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: Z20404
A;Accession: T27681
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local (
276 FRKMFYVKK
                                                                                                                                                                                                                                                       122 HTVPLSDGGKAFCIIYSVIGIPFTLLFLT----AVVQRITVHVTRRPVLYFHIRWGFSKQ 177
                                                                                                                                                                                                                                                                                                                                                                                                 137 LIFATVAYIIAGAYLFTKIEHQAELDRYQSYHTIYR---
                                                                                                                                                                                                                                                                                                                                                                                                                                        26 LVLGYLLYLVFGAVVFSSVELFYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 QKK 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 VYLETFC-ELHELKKFRKMFYV-KKDKDE------DQVHIIEHDQLSFSSITDQAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 LREKCSKOKYSVISSKODKNKEGDLNLDHLENYISIPIFLIVAILLSYITFG-----AV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 FTTTLLTTIGYGNLTPVTGRGKLLCILYALFGVPLILITVADIGKFLSENIVQLYTWYRK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 MKE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 FASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFH 169
                                                                                                                                                   VVAIVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGY
                              -----LHPVGTVEYMLCSIVFIFIGLILTTLAVDVSGSVGIAKMHSIGRGFDAMKMLNA 392
                                                                                                                                   LLVLV--FLLGYMTIS--
                                                                                                                                                                                                                 NLIPISTGGKIFCVGYAIFGIPLTLVTIADLAKFVADMLIMDPTEDPKT-----GRQ
                                                                                                                                                                                                                                                                                                       SNRSVADVENLIDTFTSINFRAFKEGLKPTDFLVPQETSRWSMISAIFFTTTVLTSIGYG
                                                                                                                                                                                                                                                                                                                                               SNYGVSVLSN----ASGNW------NWDFTSALFFASTVLSTTGYG 121
                                                                                NOKFRELYKIGITCYLL-----LGLIAMLVVLET-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SITTMCIDLVGIQYIRKMHYFGRAIKDARFALVNVGGKMVHV--PDLMRYASVLQQKYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLSMWE-GWDFFSGFYFSFITMTTVGFGDIVPLK-----REYYILDL-CYIIIGL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library, March 1996
                                                                                                                           ACVYTILEPMWSFLDSFYFCLVSLLTVGFGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 295; DB 2;
Pred. No. 2.8e-18;
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                                                                              ----FCELHELKK 275
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                                                                                                                           338
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LRKKETVKK

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R;Hembry, C. submitted to the EMBL Data A;Reference number: Z19188 A;Accession: T19860
                                                                                                                                                                                                                                                                                                         hypothetical protein C40C9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #t.C;Accession: T19860
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A; Introns: 13/3; 90/2;
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                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-334 <WIL>
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A; Residues: 1-443 <WIL>
A; Introns: 34/1;
                        A; Map position: X
                                              A; Gene: CESP:C40C9.1
                                                                                        A; Experimental source:
                                                                                                                 A; Cross-references: EMBL: 270266; PIDN: CAA94204.1; GSPDB: GN00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                      Status: preliminary; translated from
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Best Local Similarity
Matches 94; Conserv
                                                                       Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 MFYVKKDKDEDQVHIIEHDQLSFSSITDQAAGMKEDQK----QNEPFVATQSSACVDG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHFCLSEQQLEQFLGRVLEA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STYEAGRNDEKTPHI - - HQTLPTSLGVLQCFSPDEEKKTDYSERSLSRSTQTSLSLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIYPMTDAGRMLTMIFALFGIPLMLLVLQDFGKLLTITMKFPWFQTKR--LMRRIMRCCT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIIVFLIYCISGGLVFWLIEEPYQ----SELRDAWQHKIENNR---TARVDAMMKKIFNN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQPİEEMKEIERQERHDLDIFDLPLPVGIALIVTWIFICSFVLSVWDHNWTLLESFYFFF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHV-----TRRPVLYFHIRWGFS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDYLIYIKGNTSQRLTTFFIEELGSYENQLGVKWSQQKMDWD:TWNAVLFAGTICTTIGYG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNYGVSVLSNASG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.8%; Score 294.5; DB 2; llarity 26.3%; Pred. No. 3.3e-18; Conservative 63; Mismatches 124;
60/2;
                                                                                                                                                                                                                                                                                                                                  #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149/1; 222/3; 290/3
98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3
                                                                                             clone C40C9
                                                                                                                                                                                                                                                          Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RLLITMFGFILVGLSLVSMVINL-----LQAKMK 292
                                                                                                                                                                                                                                                             March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NW-----NWDETSALFFASTVLSTTGYG 121
                                                                                                                                                                                        GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77;
                                                                                                                   CESP: C40C9.1
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probable potassium channel chain n2P38 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change
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R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, I
A;Description: Potassium channels in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable potassium channel chain n2P20 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change
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                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: AF083646; PIDN: AAC32857.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-364 <WAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z22450
A; Accession: T43361
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Best Local S
Matches 71
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Best Local Similarity
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                                                                                                                                                                   255 LGL 257
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                                                                                                                                                                                                                                                                                                LLFLTAVVQRITVHVTR-----RPVLYFHIRWGFS-KQVVAIVHAVL----LGFVTVSCF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGL 257
                                                                                                                                                                                                                                                                               LIMFQSIGERVNTFIAYSLHKFRDSLH----QQGFTCLQEVTPTHLLMVSLTIGFMVIVSG
                                                                                                                                                                                                                                                                                                                                                   --IAIKSIPQQAG-YQWQFAGAFYFATYVITTVGYGHSAPSTNAGKLFCMIFALFGVPMG 124
                                                                                                                                                                                                                                                                                                                                                                        SNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFT 145
                                                                                                                                                                                                                                                                                                                                                                                                                            LILSTFTYLLFGAMVFDKLESEKDTWVRDEIERITDRLKHKYN-FSERDLHLF-----EA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIMFQSIGERVNTFIAYSLHKFRDSLH----QQGFTCLQEVTPTHLLMVSLTIGFMVIVSG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLFLTAVVQRITVHVTR-----RPVLYFHIRWGFS-KQVVAIVHAVL----LGFVTVSCF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --IAIKSIPQQAG-YQWQFAGAFYFATVVITTVGYGHSAPSTNAGKLFCMIFALFGVPMG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LILSTFTYLLFGAMVFDKLESEKDTWVRDEIERITDRLKHKYN-FSERDLHLF-----EA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEA 85
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 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.8%;
29.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 294; DB 2; 1
Pred. No. 2.9e-18;
56; Mismatches . 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   August 1998
n C. elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 364;
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                                                                                                                                                                                                                                                                         A; Gene: twk-23; CESP:F34D6.3
A; Map position: 2
                                                                                                                                                                                                                                                                                                                A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                             K;Murray, J.; Wohldmann, P.; O'Neal, D. submitted to the EMBL Data Library, Sep A;Description: The sequence of C. elega Reference number: Z21153
                                                                                                                                                                                                                                                                                                                                                                                                                                                              outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T32347
                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: T32347
                                                                                                                                                                                   Query Match
Best Local S
Matches 85
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R;Mang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Description: Potassium channels in C. elegans.
A;Reference number: Z22450
A;Accession: T43509
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: I-329 <MAN>
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                                                                                                                                                                                                                                                                                                          Genetics
                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:F34D6.
Experimental source: strain Bristol N2; clone F34D6
                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
lesidues: 1-336 <MUR>
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Best Local S
Matches 80
                                  140
                                                               8
                                                                         80 GRVLEASNYGVSVLSNASGNWNWDETSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSV 139
                                                                                                        11 LIVCTLTYLLVGÅAVFDALETENEILQVRGLGEPRKLVQRVREKLKTKYNNSNADYE---
                                                                                                                                                         26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 MLVVLETFCELHELKKFRKMFYVKKDKDEDQVHII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 ILFGLTVISAAMNLLVLRFLTMNTEDERRDEQEAI
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IGIPETLLELTAVVQRITVHVTRRPVLYEHIRWGESKQVVAIVHAVLLGEVT--VSCEFE 197
                                            --ILEATI--VKSVPHKAG-YQWKFSGAFYFATTVITTIGYGHSTPMTDAGKVFCMLYAL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
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                                                                                                                           SVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITC----YLLLGLIA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIMFQSIGERMNTFAAK---LLRFIRRAAGKQPI-VTSSDLIIFCTGWGGLLIFGGAFMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVT--VSCFFFIPAAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNYGVSVLSNASGNWNWDETSALEFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIVCTLTYLLVGAAVFDALETENEILQRKLVQRVREKLKTKYN-MSNADYE----ILEA
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                                                                                                                                                                                                Similarity
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                                                                                                                                                                                Conservative
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                                                                                                                                                                                           16.2%;
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29.1%;
                                                                                                                                                                            54;
                                                                                                                                                                       Score 284.5; DB 2;
Pred. No. 1.8e-17;
74; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                                                                                                                                                                     elegans cosmid F34D6
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Pred. No. 4.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                  September 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
                                                                                                                                                                                                     Length 336;
                                                                                                                                                                         Indels
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                                                                                                                                                                       35;
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                                                                                                                                                                    Gaps
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                                                                                                                                                                   11;
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A; Noticus, France, DNA
A; Molecule type; DNA
A; Residues: 1-475 <WIL>
A; Cross references: EMBL: 268222; PIDN:CAA92504.1; GSPDB:GN00022; CESP:ZK1251.
                                                                                                                                          Submitted to the EMBL Data A; Reference number: Z20411
                                                                                                                                                                                        hypothetical protein ZK1251.8 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tes C:Accession: T27725
                                                                                                                                                                                                                                                                       RESULT
T27725
                                                                                                   A; Status: preliminary; translated from
                                                                                                                         A; Reference number:
A; Accession: T27725
                                                                                                                                                                               R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                           Дb
                                                                                                                                                                                                                                                                                                                                                                         Qγ
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A; Residues: 1-1001 <GG
A; Cross-references: El
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: ORK1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potassium channel protein - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 77
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                                                                                                                                                                                                                                                                                                                                                                                       185 -- IALFILLPSWVFTYFE-NWPYSISLYYSYVTTTTIGFGDYVPTFGANQPKEFGGWFVV
                                                                                                                                                                                                                                                                                                                                         242
                                                                                                                                                                                                                                                                                                                                                               245 YKIGITCYLLLGLIAMLVVLETF
                                                                                                                                                                                                                                                                                                                                                                                                                       190 VTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQK-----FREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 GIPVNGILFAGLGEYFGRTFEAIYRRYKKYKNSTDMHYVPPQLGL---ITTVVIALIPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 GIPET-LLE------LTAVVQRITVHVTRRPVLYEHIRWGESKQVVAIVHAVLLGE 189
                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 VLEASNYGVSVLSNASGN-WNWDETSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
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nes 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228
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                                                                                                                                                                                                                                                                                                                                    YQIFVIVWFIFSL-GYLVMIMTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNISPTTFAGRMIMIAYSVI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLIFYISYLMFGAAIYYHIEHGEEKISRAEQRKAQIAINEYLLEELGDKNTTTQDEILQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVLGYLLYLVFGAVVFSSVELPYEDLLRQELRK-----LKRRFLEEHECLSEQOLEQFLGR 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFSLVFILFGLTVISAAMNLLVLRFLTMNTEDERRDEQEAI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLGLIAMLVVLETFCELHELKKFRKMFYVKKDKDEDQVHII
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| GGAFMESSYE-WWTYFDAVYYCFVTLTTIGFGDYV-----ALQKRGSLQTQPEYV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPAAVFSYLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITC----YL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGIPLGLIMFQSIGERMNTFAAK----LLRFIRRAAGKQPI-VTSSDLIIFCTGWGGLLIF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <GOL>
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                                                                                                                                                        Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.1%;
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                                                                                                                                                                                                                                                                                                                                  263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 264.5; DB 2
Pred. No. 3.8e-15;
                                                                                                                                                        December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                     #text_change
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A;Cross-references: EMBL:Z75543; PIDN:CAA99871.1; GSPDB:GN00023; CESP:K01D12.4 A;Experimental source: clone K01D12 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-383 <WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein K01D12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Introns: 28/3;
                                                                                                                                                                                                                                                                  A;Gene: CESP:K01D12.4
A;Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z19703
A; Accession: T23182
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T23182
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A; Introns: 13/3; 47/2; 89/3; 178/1; 245/3; 311/2; 366/3; 419/2
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                                                                                                                                                    Matches
                                                                                                                                                                                        Query Match
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Best Local Similarity
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 101
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                                                                                                                                               / Match 14.3%; Score 251; DB 2; I
Local Similarity 25.8%; Pred. No. 1.8e-14;
Construction 63; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 LGDQFNIPEEELANFDMSAFVDNAIKVEKGE 459
                                                                       44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
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                                   77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFTLL-----FLTAVVQRITVHVTR------171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKNKEEEKDVIDETPAE-KWSIGNSVIFAFTVITTIGYGHVAPETFEGRLFLIFYGVIGV 201
                 FGFLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLE-----EHECLSEQQLE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --DQVHIIEHDQLSF--SSITDQAAGMKEDQ 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITFTCYLVAGAKILSVYEPEMDFFKALYFNEVTLTTIGLGDEVP-KSFDYLLITLIXIGI 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIAGVAVYTVFGALSMQWLESPDRVRALLKRELKPVESLPPPPSISGLPDRITRVYLGEE 82
EMVRFISDGATSG--LLNSRS---RFDHLGSLFFSATVISTIGFGTSTPRTHLGRFITIV 155
                                                                       FVLICIILIVYLAFGAILFHWLE--WENEVDERI-AIDNRMADYQKVYCKHKPLNECDFE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCYLLLGLIAMLVVLETFCELHELKKFRKMFYVKKDKDE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VWNTGKEMKEMSMRTAREPGEGDEIEVIENGNDENGKEEDEEEPENNEPRKTEESIALG- 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -WGFSKQV-----HAVLLGF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFTLLTIADLGMFLTRFLKNLLTMARRFAHYLVKLYQKAKKQRNKSQKTSPVMPDSERSE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VSVLSNASGNWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAILDPGVHECLERTILTLFHDTKCDPYSFEHLNIELIDRCYAEANVPIPEGYGGQPRKK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----HECLSEQQLEQF------LGRVLEASN-----YG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GLALTTMAIEIAADL-----LKKLHYIGRKMENVGQA;VVWFGGKKMTMKSLVKH 428
                                                                                                                                                                                                                                                76/3; 184/2; 217/2; 270/2; 295/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          June 1996
                                                                                                                                                                                                                                                                                                                                                                                                     GB/EMBL/DDBJ
                                                                                                                                                                                    Length 383;
                                                                                                                                                    Indels 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T24265
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A; Introns: 95/3; 142/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-522 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T24265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A; Reference number: Z19866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Wilkinson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T01B4.1 - Caenorhabditis elegans
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T24265
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Matches
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                                                                                          287 -- DEDQVH
                                                                                                                                                                                                           239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216
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                                                        343 KADKNDMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 YGVVGCTCCVLFFNLFLERLVTGMSYILRSLRERKIRYRLKESGNKPVTLLLNNEDFNES
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mes 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVSC-----FFFI-----PAAVFSVLEDDWNFLESFYFCFISLSTI 226
                                                                                                                                                                    GEGYNQ-KFRELYKIGITCYLLLGLIAMLVVLETFCELHEL-----KKFRKMFYVKKDK 286
                                                                                                                                                                                                                                                                                  CVKWAKKIQFNVQQCLKKCFGRKQKRASSLASITSKEMLEVFFEVPEDDKEDTTFQLRWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKIISRQRSQETWGQWFVRVVETLSELLGIRYIMLILIILGYACLGGYMFQALEYDQQQL 66
                                                                                                                                                                                                         L---LVIVLEVVLCSEV-VSFW----
                                                                                                                                                                                                                                                                                                                                                            RGEGWRWDFWNSVFFSATIFTTIGYGNLACKTNLGRIATIIYGMIGIPLMLFVLKNFGEL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEASNYGVS-----VLSNA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFGDYVSNQQDVTRMSPDLYRFVNFCLLTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSSCGGHMDNWRPSVYKVFFILFSMCLVLITASAGIYSVVE-NWNYIDSLYFCFISFATI
                                                                                                                               DHPRTACALFVLYFIGLALFAMVYAILQERVENQYMWALELIDQKYQEKLKQDMYDEDEK
                                                                                                                                                                                                                                                                                                                       -----VQRI-----YFHIRWG 173
                                                                                                                                                                                                                                                                                                                                                                                               -SGNWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAV---
                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ELEAEKRVRLSESSLLAVNLLEH-----LKQMNCGQSNEKRCLELITKTFIQRSDEE 118
                                                                                             292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224/3; 290/1; 458/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.0%; Score 246; DB 2;
24.7%; Pred. No. 7.4e-14;
tive 54; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               March
                                                                                                                                                                                                           -----ENWDFLTAFYFFFVSLSTIGFGDIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                  238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215
                                                                                                                                                                                                         282
                                                                                                                                                                                                                                            233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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hypothetical protein W06D12.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-513 <NEL>
                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, July 1996 A:Description: The sequence of C. elegans cosmid C52B9. A;Reference number: Z20545 A;Accession: T28933
                                                                                                 A; Map position: X
                                                                                                                                             A;Cross-references: EMBL:U64598; PIDN:AAC47976.1; GSPDB:GN00028; CESP:C52B9.
A;Experimental source: strain Bristol N2; clone C52B9
                                                                                                                                                                                                                                                                                                                                                  C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
                                                                                 A; Introns: 12/3; 54/3;
                                                                                                                       A;Gene: CESP:C52B9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
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       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESD:W06D12.5
A;Map position: 5
A;Introns: 4/3; 50/1; 89/2; 153/1; 244/3; 285/3; 333/1; 384/2; 509/1; 553/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: clone w06D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-631 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, November 1996 A; Reference number: Z20177 A; A; Accession: T26232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL;282073; PIDN:CAB04926.1; GSPDB:GN00023; CESP:W06D12.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T26232
R;Basham, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              529 VKPEDRPSTPKV--QRALSVD 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 MKEDQKQNEPFVATQSSACVD 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 YLLLGL-IAMLVVLETFCELHELKKFRKMFYVKKDKDEDQVHIIEHDQLSFSSITDQAAG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 DELSGPEPGTGMDMFLCFYFSFISLSTIGLGDIMPNNATVGNNRNIYENEKIKFAPIISI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 AH---GIQKFRELNGNKHVDEDEIISLPIKACLLLLASYLGACTIFIYFY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 FHIRWGFSK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 LFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 LAENITESVNNINTTTTEEEMKVYIREAYIELMKLEGQYKGSTYYKLEADDNWKWTFESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 KSMYWFAFHRKQIGFRHFSVVILVLLYTLLGAVMFWTVESRHEKAKTLDHVNNLEHLLDR 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 RSAWCFGF-----LVLGYLLYLVFGAVVFSSVE-----LPVEDLLRQELRK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
mes 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFFFGMAVTKVVNRNTFIAV-ENGIFGAFTLVENKLD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDWNFLE-----SFYFCFISLSTIGLGDYVPGE---GYNQKFRELYKIG----ITC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFFSMNVYTTTGYGSIAPESTLGQVLVCVYGFIFVPVTLVVLRDLGQFFLVHLTK---LY 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKRRFLEE----HECLSEQQLEQFLGRV-----LEASNYGVSVLS-NASGNWNWDFTSA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                             90/3; 158/1; 173/1; 227/3; 299/3; 346/2; 378/2; 405/1; 452/3
     13.9%;
22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.0%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 ------QVVAIVHAVLLGFVTVSCFFFIPAAVFSVLE
Score 244; DB 2;
Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 245; DB 2; I
Pred. No. 1.1e-13;
52; Mismatches 130;
             Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -AIVTRSSAS 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423
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                                                                                                                                                                                                                                                                                            망
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                                                                                                                                                                                                                                                                                                                                                 Matches
339 YIIFGL----SLATMCIDLAGTEYIRKIHYLGTKMEDAKGAVMTGLQAGEHLLKH
                          252 YLLLGLIAMLVVLETFC-ELHELKKFRKMFYVKKDKDEDQ------VHIIEH 296
                                                                   296 FLF--
                                                                                               195
                                                                                                                           236
                                                                                                                                                      179
                                                                                                                                                                180 ITVTGRVACIIFALLGIPLLLVTIADIGKFLSEFLS---YLYRSYR-GFKRKLRRQSKKI 235
                                                                                                                                                                                                           126
                                                                                                                                                                                                                     120 YRNOFITAKHLLNKTREDEVLWTFPNSMFFAATVITTIVQVKNRSGNRVVFSRGYGNLVP 179
                                                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                     26
                                                                        FFFIPAAVFSVLEDDW----NFLESFYFGFISLSTIGLGDYVPGEGYNQKFRELYKIGITC
                                                                                                             {\tt TSQYRSQSQSRSSSYMGSSKAGSMNLHDIDSDSEDSAGDELRIPYFMVLLVLLAYTAIGG}
                                                                                                                                                                                           LSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQV----- 178
                                                                                                                                                                                                                                                                                                      LVLGYLLYLVFGAVVFSSVELFYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEA 85
                                                                                                                                                                                                                                           -SNYGVSV--LSNASGNWN--WDFTSALFFASTVLST-----
                                                                                                                                                                                                                                                                            LVILLELYLIAGAFLFRYLEAPKE--LEDSDNRISR---EAFNAINQEYFEQLVKNMFQA 119
                                                                                                                                                                                                                                                                                                                                                81;
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                      -QSWEHLEYFEAFYFCFITMATVGFGDIVPNE-----QVYVFFTMA
                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                      -----VAIVHAVLLGFVTVSC
                                                                                                                                                                                                                                                                                                                                        95;
                                                                                                                                                                                                                                                                                                                                    Indels 116;
                                                                                                                                                                                                                                                   ----TGYGHTVP 125
  389
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                       194
                                                                                  251
                                                                                                              295
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